



-48-

SEQUENCE LISTING

(1) GENERAL INFORMATION

- TU500
- (i) APPLICANT: Ullrich,, Axel
Gishizsky,, Mikhail
Sures,, Irman G.
- (ii) TITLE OF THE INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TYROSINE KINASES
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York,
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: Patentin, Ver 1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/426,509
(B) FILING DATE: 21-APR-1995
(C) CLASSIFICATION:
- C 1
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/232,545
(B) FILING DATE: 22-APR-1994

- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Coruzzi, Laura A
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 7683-0074-999

- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-790-9090
(B) TELEFAX: 212-869-9741
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGCTCCAA	GTTGTGCAGC	CGGGACCGCC	TCGGGGTGTG	CAGCCGGCTC	GC GGAGGCC	60
TCCCTGGGGGC	GGGCGCGGGG	CGGCTCGGGG	GCGCCCCCTG	AGCAGAAAAC	AGGAAGAAC	120
AGGCTCGGTC	CAGTGGCAC	CAGCTCCCTA	CCTCCTGTGC	CAGCCGCCTG	GCCTGTGGCA	180
GGCCATTCCC	AGCGTCCCCG	ACTGTGACCA	CTTGCTCAGT	GTGCCTCTCA	CCTGCCTCAG	240
TTTCCCTCTG	GGGGCGATG	GCGGGGCGAG	GCTCTCTGGT	TTCCTGGCGG	GCATTTCACG	300

500

C

GCTGTGATTC	TGCTGAGGAA	CTTCCCCGGG	TGAGCCCCCG	CTTCCTCCGA	GCCTGGCACC	360
CCCCTCCCGT	CTCAGCCAGG	ATGCCAACGA	GGCGCTGGC	CCCAGGCACC	CAGTGTATCA	420
CCAAATGCGA	GCACACCCGC	CCCAAGCCAG	GGGAGCTGGC	CTTCCGCAAG	GGCGACGTGG	480
TCACCATCCT	GGAGGCCTGC	GAGAACAAAGA	GCTGGTACCG	CGTCAAGCAC	CACACCAGTG	540
GACAGGAGGG	GCTGCTGGCA	GCTGGGGCGC	TGCGGGAGCG	GGAGGCCCTC	TCCGCAGACC	600
CCAAGCTCAG	CCTCATGCCG	TGGTTCCACG	GGAAGATCTC	GGGCCAGGAG	GCTGTCCAGC	660
AGCTGCAGCC	TCCCAGGGAT	GGGCTGTTCC	TGGTGCGGGA	GTCCGCGCGC	CACCCCAGGG	720
ACTACGTCTT	GTGCGTGAGC	TTTGGCCGCG	ACGTCACTCCA	CTACCGCGTG	CTGCACCGCG	780
ACGGCCACCT	CACAATCGAT	GAGGCCGTGT	TCTTCTGCAA	CCTCATGGAC	ATGGTGGAGC	840
ATTACAGCAA	GGACAAGGGC	GCTATCTGCA	CCAAGCTGGT	GAGACCAAAG	CGGAAACACG	900
GGACCAAGTC	GGCCGAGGGAG	GAGCTGGCCA	GGGCGGGCTG	GTTACTGAAC	CTGCAGCATT	960
TGACATTGGG	AGCACAGATC	GGAGAGGGAG	AGTTTGGAGC	TGTCCTGCAG	GGTGAGTACC	1020
TGGGGCAAAA	GGTGGCCGTG	AAGAATATCA	AGTGTGATGT	GACAGCCCAG	GCCTTCCTGG	1080
ACGAGACGGC	CGTCATGACG	AAGATGCAAC	ACGAGAACCT	GGTGCCTCTC	CTGGGCGTGA	1140
TCCTGCACCA	GGGGCTGTAC	ATTGTCTGAG	AGCACGTGAG	CAAGGGCAAC	CTGGTGAAC	1200
TTCTGCGGAC	CCGGGGTCGA	GCCCTCGTGA	ACACCGCTCA	GCTCCTGCAG	TTTTCTCTGC	1260
ACGTGGCCGA	GGGCATGGAG	TACCTGGAGA	GCAAGAAGCT	TGTGCACCGC	GACCTGGCCG	1320
CCCGCAACAT	CCTGGTCTCA	GAGGACCTGG	TGGCCAAGGT	CAGCGACTTT	GGCCTGGCCA	1380
AAGCCGAGCG	GAAGGGGCTA	GACTCAAGCC	GGCTGCCGT	CAAGTGGACG	GCGCCCGAGG	1440
CTCTCAAACA	CGGGAAAGTTC	ACCAGCAAGT	CGGATGTCTG	GAGTTTGAGG	GTGCTGCTCT	1500
GGGAGGTCTT	CTCATATGGA	CGGGCTCCGT	ACCCCTAAAAT	GTCACTGAAA	GAGGTGTAGG	1560
AGGCCGTGGA	GAAGGGGTAC	CGCATGGAAC	CCCCCGAGGG	CTGTCCAGGC	CCCGTGCACG	1620
TCCTCATGAG	CAGCTGCTGG	GAGGCAGAGC	CCGCCCCCG	GCCACCCCTC	CGCAAACCTGG	1680
CCGAGAAGCT	GGCCCGGGAG	CTACGCAGTG	CAGGTGCC	AGCCTCCGTC	TCAGGGCAGG	1740
ACGCCGACGG	CTCCACCTCG	CCCCGAAGCC	AGGAGCCCTG	ACCCCACCCG	GTGGGGCCCT	1800
TGGCCCCAGA	GGACCGAGAG	AGTGGAGAGT	GCGGCGTGGG	GGCACTGACC	AGGCCCAAGG	1860
AGGGTCCAGG	CGGGCAAGTC	ATCCTCCTGG	TGCCCACAGC	AGGGGCTGGC	CCACGTAGGG	1920
GGCTCTGGC	GGCCCGTGGA	CACCCAGAC	CTGCGAAGGA	TGATCGCCCG	ATAAAGACGG	1980
ATTCTAAGGA	CTCTAAAAAA					2000

(2) INFORMATION FOR SEQ ID NO:2:

- C
cont.*
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Gly	Arg	Gly	Ser	Leu	Val	Ser	Trp	Arg	Ala	Phe	His	Gly	Cys
1					5				10					15	
Asp	Ser	Ala	Glu	Glu	Leu	Pro	Arg	Val	Ser	Pro	Arg	Phe	Leu	Arg	Ala
									20				25		30
Trp	His	Pro	Pro	Pro	Val	Ser	Ala	Arg	Met	Pro	Thr	Arg	Arg	Trp	Ala
									35				40		45
Pro	Gly	Thr	Gln	Cys	Ile	Thr	Lys	Cys	Glu	His	Thr	Arg	Pro	Lys	Pro
									50				55		60
Gly	Glu	Leu	Ala	Phe	Arg	Lys	Gly	Asp	Val	Val	Thr	Ile	Leu	Glu	Ala
									65				70		75
Cys	Glu	Asn	Lys	Ser	Trp	Tyr	Arg	Val	Lys	His	His	Thr	Ser	Gly	Gln
									85				90		95
Glu	Gly	Leu	Leu	Ala	Ala	Gly	Ala	Leu	Arg	Glu	Arg	Glu	Ala	Leu	Ser
									100				105		110
Ala	Asp	Pro	Lys	Leu	Ser	Leu	Met	Pro	Trp	Phe	His	Gly	Lys	Ile	Ser
									115				120		125
Gly	Gln	Glu	Ala	Val	Gln	Gln	Leu	Gln	Pro	Pro	Glu	Asp	Gly	Leu	Phe
									130				135		140
Leu	Val	Arg	Glu	Ser	Ala	Arg	His	Pro	Gly	Asp	Tyr	Val	Leu	Cys	Val
									145				150		155
Ser	Phe	Gly	Arg	Asp	Val	Ile	His	Tyr	Arg	Val	Leu	His	Arg	Asp	Gly
									165				170		175
His	Leu	Thr	Ile	Asp	Glu	Ala	Val	Phe	Phe	Cys	Asn	Leu	Met	Asp	Met
									180				185		190
Val	Glu	His	Tyr	Ser	Lys	Asp	Lys	Gly	Ala	Ile	Cys	Thr	Lys	Leu	Val

195 200 205
Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala Glu Glu Glu Leu Ala
210 215 220
Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu Thr Leu Gly Ala Gln
225 230 235 240
Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly
245 250 255
Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
260 265 270
Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
275 280 285
Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met
290 295 300
Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
305 310 315 320
Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
325 330 335
Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
340 345 350
Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
355 360 365
Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
370 375 380
Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
385 390 395 400
Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
405 410 415
Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu
420 425 430
Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly
435 440 445
Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
450 455 460
Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
465 470 475 480
Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val Ser Gly Gln Asp Ala
485 490 495
Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro
500 505

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTTTTG CTTAGAGCTT GAGAGTCAAA GTTAAGGACC CACATGTATA CTTCGGCTCT 60
AGCGAGTCTA AGGATGATAA TATGGATACA AAATCTATTG TAGAAGAACT TCTTCTCAAA 120
AGATCACAGC AAAAGAAGAA AATGTCACCA AATAATTACA AAGAACGGCT TTTGTTTG 180
ACCAAAACAA ACCTTCCTA CTATGAATAT GACAAAATGA AAAGGGGCAG CAGAAAAGGA 240
TCCATTGAAA TTAAGAAAAT CAGATGTGTG GAGAAAGTAA ATCTCGAGGA GCAGACGCCT 300
GTAGAGAGAC AGTACCCATT TCAGATTGTC TATAAAGATG GGCTTCTCTA TGTCTATGCA 360
TCAAATGAAG AGAGCCGAAG TCAGTGGTTG AAAGCATTAC AAAAAGAGAT AAGGGGTAAC 420
CCCCACCTGC TGGTCAAGTA CCATAGTGGG TTCTTCGTGG ACGGGAAGTT CCTGTGTTGC 480
CAGCAGAGCT GTAAAGCAGC CCCAGGATGT ACCCTCTGGG AAGCATATGC TAATCTGCAT 540
ACTGCAGTCA ATGAAGAGAA ACACAGAGTT CCCACCTTCC CAGACAGAGT GCTGAAGATA 600
CCTCGGGCAG TTCCTGTTCT CAAAATGGAT GCACCATCTT CAAGTACCAC TCTAGCCCAA 660
TATGACAACG AATCAAAGAA AAACTATGGC TCCCAGCCAC CATCTTCAAG TACCAAGTCTA 720
GCGCAATATG ACAGCAACTC AAAGAAAATC TATGGCTCCC AGCCAAACTT CAACATGCAG 780
TATATTCCAA GGGAAAGACTT CCCTGACTGG TGGCAAGTAA GAAAAGTAA AAGTAGCAGC 840
AGCAGTGAAG ATGTTGCAAG CAGTAACCAA AAAGAAAAGAA ATGTGAATCA CACCACCTCA 900
AAGATTCAT GGGATTCCC TGAGTCAAGT TCATCTGAAG AAGAGGAAAA CCTGGATGAT 960

TATGACTGGT	TTGCTGGTAA	CATCTCCAGA	TCACAATCTG	AACAGTTACT	CAGACAAAAG	1020
GGAAAAGAAG	GAGCATTAT	GGTTAGAAAT	TCGAGCCAAG	TGGGAATGTA	CACAGTGTCC	1080
TTATTTAGTA	AGGCTGTGAA	TGATAAAAAA	GGAACTGTCA	AACATTACCA	CGTGCATACA	1140
AATGCTGAGA	ACAAATTATA	CCTGGCAGAA	AACTACTGTT	TTGATTCCAT	TCCAAAGCTT	1200
ATTCAATTATC	ATCAACACAA	TTCAGCAGGC	ATGATCACAC	GGCTCCGCCA	CCCTGTGTCA	1260
ACAAAGGCCA	ACAAGGTCCC	CGACTCTGTG	TCCCTGGAA	ATGGAATCTG	GGAACTGAAA	1320
AGAGAAGAGA	TTACCTTGTT	GAAGGAGCTG	GGAAAGTGGCC	AGTTTGGAGT	GGTCCAGCTG	1380
GGCAAGTGGA	AGGGGCAGTA	TGATGTTGCT	GTAAAGATGA	TCAAGGAGGG	CTCCATGTCA	1440
GAAGATGAAT	TCTTTCAGGA	GGCCCAGACT	ATGATGAAAC	TCAGCCATCC	CAAGCTGGTT	1500
AAATTCTATG	GAGTGTGTT	AAAGGAATAC	CCCATATACA	TAGTGACTGA	ATATATAAGC	1560
AATGGCTGCT	TGCTGAATTA	CCTGAGGAGT	CACGGAAAAG	GACTTGAACC	TTCCCAGCTC	1620
TTAGAAATGT	GCTACGATGT	CTGTGAAGGC	ATGGCCTTCT	TGGAGAGTCA	CCAATTCTATA	1680
CACCAGGACT	TGGCTGCTCG	TAACTGCTTG	GTGGACAGAG	ATCTCTGTGT	GAAAGTATCT	1740
GACTTTGGAA	TGACAAAGGT	TGTTCTTGAT	GACCAGTATG	TCAGTTCACT	CGGAACAAAG	1800
TTTCCAGTCA	AGTGGTCAGC	TCCAGAGGTG	TTTCATTACT	TCAAATACAG	CAGCAAGTCA	1860
GACGTATGGG	CATTTGGGAT	CCTGATGTGG	GAGGTGTTCA	GCCTGGGGAA	GCAGCCCTAT	1920
GACTTGTATG	ACAACTCCC	GGTGGTTCTG	AAGGTCTCCC	AGGGCCACAG	GCTTTACCGG	1980
CCCCACCTGG	CATCGGACAC	CATCTACCAAG	ATCATGTACA	GCTGCTGGCA	CGAGCTTCCA	2040
GAAAAGCGTC	CCACATTCA	GCAACTCCTG	TCTTCCATTG	AACCACTTCG	GGAAAAAGAC	2100
AAGCATTGAA	GAAGAAATTA	GGAGTGCTGA	TAAGAATGAA	TATAGATGCT	GGCCAGCATT	2160
TTCATTCAATT	TTAAGGAAAG	TAGCAAGGCA	TAATGTAATT	TAGCTAGTTT	TTAATAGTGT	2220
TCTCTGTATT	GTCTATTATT	TAGAAATGAA	CAAGGCAGGA	AACAAAAGAT	TCCCTTGAAA	2280
TTTAGGTCAA	ATTAGTAATT	TTGTTTATGC	TGCCCTGTAT	ATAACACTTT	CCAGCCTATA	2340
GCAGAACAC	ATTTCAGAC	TGCAATATAG	AGACTGTGTT	CATGTGTAAA	GACTGAGCAG	2400
AACTGAAAAA	TTACTTATTG	GATATTCAATT	CTTTTCTTTA	TATTGTCATT	GTCACAAACAA	2460
TTAAATATAC	TACCAAGTAC	AAAAAAAAAA	AAAAAAAAAA			2500

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Thr Lys Ser Ile Leu Glu Leu Leu Lys Arg Ser Gln
1 5 10 15
Gln Lys Lys Lys Met Ser Pro Asn Asn Tyr Lys Glu Arg Leu Phe Val
20 25 30
Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu Tyr Asp Lys Met Lys Arg
35 40 45
Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys Lys Ile Arg Cys Val Glu
50 55 60
Lys Val Asn Leu Glu Glu Gln Thr Pro Val Glu Arg Gln Tyr Pro Phe
65 70 75 80
Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr Val Tyr Ala Ser Asn Glu
85 90 95
Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu Gln Lys Glu Ile Arg Gly
100 105 110
Asn Pro His Leu Leu Val Lys Tyr His Ser Gly Phe Phe Val Asp Gly
115 120 125
Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys Ala Ala Pro Gly Cys Thr
130 135 140
Leu Trp Glu Ala Tyr Ala Asn Leu His Thr Ala Val Asn Glu Glu Lys
145 150 155 160
His Arg Val Pro Thr Phe Pro Asp Arg Val Leu Lys Ile Pro Arg Ala
165 170 175
Val Pro Val Leu Lys Met Asp Ala Pro Ser Ser Ser Thr Thr Leu Ala
180 185 190
Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr Gly Ser Gln Pro Pro Ser
195 200 205
Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser Asn Ser Lys Lys Ile Tyr
210 215 220

59

Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr Ile Pro Arg Glu Asp Phe
225 230 235 240
Pro Asp Trp Trp Gln Val Arg Lys Leu Lys Ser Ser Ser Ser Glu
245 250 255
Asp Val Ala Ser Ser Asn Gln Lys Glu Arg Asn Val Asn His Thr Thr
260 265 270
Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser Ser Ser Glu Glu Glu
275 280 285
Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala Gly Asn Ile Ser Arg Ser
290 295 300
Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly Lys Glu Gly Ala Phe Met
305 310 315 320
Val Arg Asn Ser Ser Gln Val Gly Met Tyr Thr Val Ser Leu Phe Ser
325 330 335
Lys Ala Val Asn Asp Lys Lys Gly Thr Val Lys His Tyr His Val His
340 345 350
Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala Glu Asn Tyr Cys Phe Asp
355 360 365
Ser Ile Pro Lys Leu Ile His Tyr His Gln His Asn Ser Ala Gly Met
370 375 380
Ile Thr Arg Leu Arg His Pro Val Ser Thr Lys Ala Asn Lys Val Pro
385 390 395 400
Asp Ser Val Ser Leu Gly Asn Gly Ile Trp Glu Leu Lys Arg Glu Glu
405 410 415
Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly Gln Phe Gly Val Val Gln
420 425 430
Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val Ala Val Lys Met Ile Lys
435 440 445
Glu Gly Ser Met Ser Glu Asp Glu Phe Phe Gln Glu Ala Gln Thr Met
450 455 460
Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser
465 470 475 480
Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys
485 490 495
Leu Leu Asn Tyr Leu Arg Ser His Gly Lys Gly Leu Glu Pro Ser Gln
500 505 510
Leu Leu Glu Met Cys Tyr Asp Val Cys Glu Gly Met Ala Phe Leu Glu
515 520 525
Ser His Gln Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val
530 535 540
Asp Arg Asp Leu Cys Val Lys Val Ser Asp Phe Gly Met Thr Arg Tyr
545 550 555 560
Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val
565 570 575
Lys Trp Ser Ala Pro Glu Val Phe His Tyr Phe Lys Tyr Ser Ser Lys
580 585 590
Ser Asp Val Trp Ala Phe Gly Ile Leu Met Trp Glu Val Phe Ser Leu
595 600 605
Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys
610 615 620
Val Ser Gln Gly His Arg Leu Tyr Arg Pro His Leu Ala Ser Asp Thr
625 630 635 640
Ile Tyr Gln Ile Met Tyr Ser Cys Trp His Glu Leu Pro Glu Lys Arg
645 650 655
Pro Thr Phe Gln Gln Leu Leu Ser Ser Ile Glu Pro Leu Arg Glu Lys
660 665 670
Asp Lys His
675

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGGACTGGT CGAAAGACAG GAACAGACTT GAAACAGGGG GAGAGCTCCT GGCAGAACGA 60
AGACGTGGAG GTTTTACCAAG GGATAAGAAG AAAAGACACC TTCCTAGTGA GCAGCTGCC 120
AGCTCCTGCT CAGTTTGCC TCGGGTAGC ACCTCCAGCC ACAGAAAGCA AGCCGGTAAG 180
TCTCTCCAGG TAGGACTTGC TGCAACCCAG CTGCTGGACT GATCTGAAAC GGGACTTTGC 240
ATACTCTCCG AAGTATGGTG AGTTGGTGCT GACTTCAAAG TTGCCTGGTG AAGGAAGATA 300
AGGTGGATCG CAGAGACTAA GGGGAGAGGG AGAACGCCCTG CTCCTCTTCT CCCCACCAAG 360
GCACAATGAG CAACATCTGT CAGAGGCTCT GGGAGTACCT AGAACCCCTAT CTCCCCTGTT 420
TGTCCACGGA GGCAGACAAG TCAACCGTGA TTGAAAATCC AGGGGCCCTT TGCTCTCCCC 480
AGTCACAGAG GCATGGCCAC TACTTTGTGG CTTTGTGTTGA TTACCAAGGCT CGGACTGCTG 540
AGGACTTGAG CTTCCGAGCA GGTGACAAAC TTCAAGTTCT GGACACTTTG CATGAGGGCT 600
GGTGGTTTGC CAGACACTTG GAGAAAAGAC GAGATGGCTC CAGTCAGCAA CTACAAGGCT 660
ATATTCCCTC TAACTACGTG GCTGAGGACA GAAGCCTACA GGCAGAGCCG TGGTTCTTG 720
GAGCAATCGG AAGATCAGAT GCAGAGAAAC AACTATTATA TTCAAGAAAAC AAGACCGGTT 780
CCTTTCTAAT CAGAGAAAGT GAAAGCCAAA AAGGAGAATT CTCTCTTCA GTTTAGATG 840
GAGCAGTTGT AAAACACTAC AGAATTAAAA GACTGGATGA AGGGGGATT TTTCTCACGC 900
GAAGAAGAAT CTTTCAACA CTGAACGAAT TTGTGAGCCA CTACACCAAG ACAAGTGACG 960
GCCTGTGTGT CAAGCTGGGG AAACCATGCT TAAAGATCCA GGTCCCGAGCT CCATTTGATT 1020
TGTCTATAA AACCGTGGAC CAATGGGAGA TAGACCGCAA CTCCATACAG CTTCTGAAGC 1080
GATTGGGATC TGGTCAGTTT GGCGAAGTAT GGGAAAGGTCT GTGGAACAAT ACCACTCCAG 1140
TAGCAGTGAA AACATTAAAA CCAGGTTCAA TTATCCAGCT TTATGCTGTT TGCACTTTAG 1200
AGATAATGAA GAACCTAAGA CATCCAAAGC TGAGACATGG AAGTCTGCAA GAATATCTCC 1260
AAGATCCAAT TTATATTATT ACAGAGTTGA CTCAACAGGT AGACATGGCG GCACAGGTTG 1320
AAAATGACAC TGGATCAAAA ATCCATCTGA CCTCTGGAAT GGCCTATCTG GAGTCTCGGA 1380
ATGTCCTCGT TGGTGAACAT AATATCTACA AAGTAGCAGA TTTTGGACTT GCCAGAGTTT 1440
TTAAGGTAGA TAATGAAGAC ATCTATGAAT CTAGACACGA AATAAAGCTG CCGGTGAAGT 1500
GGACTGCGCC CGAAGCCATT CGTAGTAATA AATTCAAGCAT TAAGTCCGAT GTATGGTCAT 1560
TTGGAATCCT TCTTTATGAA ATCATTACTT ATGGCAAAAT GCCTTACAGT GGTATGACAG 1620
GTGCCAGGT AATCCAGATG TTGGCTAAA ACTATAGACT TCCGCAACCA TCCAACGTGC 1680
CACAGCAATT TTACAACATC ATGTTGGAGT GCTGGAATGC AGAGCCTAAG GAACGACCTA 1740
CATTGAGAC ACTGCGTTGG AAAACTGAAG ACTATTTGA AACAGACTCT TCATATTCAAG 1800
ATGCAAATAA CTTCATAAGA TGAACACTGG AGAAGAATAT CAAATAATAA AGTAGCAAAA 1860
CAAATTCAAA TAATCCATTG CAAAATACAA TGTTATCAAC CAACTGCACA ATCAGTTTAT 1920
CCTGACATAT TCAAGTGATA GGATAAAAGTT GGCCATGTAT TATGAAAAAG ATTATTTGTG 1980
CATTTTATTG ACTGGGCAAC ACTGCAGGAC AGTCAAGGTC ATATATAATT GCTCACTGCC 2040
TGGAAAATTA AGCACACTAA ACCAAGTTAT TTTTCTTTT AAGAGATACT TACATTCCA 2100
TTTATTGTTT GAAATGTCGC GATCAAGAGA ATCAACAGAT GATAGTCCAA TTTTACTCA 2160
GTGATGACTG TGTAGCATT TCCGTGTTAC TGATTAGAGT GGTTATTCACT TATTCTCTAG 2220
ATTGCTGAAT CCCATCAGGC TGTTATTATG AAGGAATTG ATTGCTTGC TGACAGCAG 2280
GACCTGTGCT TTGAGATTTC TTTTCTCTT TTAAATATC CTGTAACATC AATGATGGTA 2340
AAGCCATGTT AAATGACTTG ATTGTACTTG GAGTAATTGC ACATTTTTT CTATGCATAA 2400
AAAAATGATG CAGCTGTTGA GAAAACGAAG TCTTTTCAT TTTGCAGAAG GAAATGATGG 2460
AATTTTCTG TACTTCAGTA TGTGTCAACT GAGAGTCATA TACATTAGTT TTAATCTCTT 2520
AATATTGAGA ATCAGGTTGC AAAACGGATG AGTTATTATC TATGGAAATG TGAGAAATGT 2580
CTAATAGCCC ATAAAGTCTG AGAAATAGGT ATCAAAATAG TTTAGGAAAA TGAGAGGAGA 2640
ACAGTAGGAT TGCTGTGGCC TAGACTTCTG AGTAATTAAT AAAGAAAAAG AAGTACCAAA 2700
AAAAAAAAAA 2760
2770

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Asn Ile Cys Gln Arg Leu Trp Glu Tyr Leu Glu Pro Tyr Leu
1 5 10 15
Pro Cys Leu Ser Thr Glu Ala Asp Lys Ser Thr Val Ile Glu Asn Pro
20 25 30
Gly Ala Leu Cys Ser Pro Gln Ser Gln Arg His Gly His Tyr Phe Val

35 40 45

Ala Leu Phe Asp Tyr Gln Ala Arg Thr Ala Glu Asp Leu Ser Phe Arg
50 55 60

Ala Gly Asp Lys Lys Leu Gln Val Leu Asp Thr Leu His Glu Gly Trp
65 70 75 80

Trp Phe Ala Arg His Leu Glu Lys Arg Arg Asp Gly Ser Ser Gln Gln
85 90 95

Leu Gln Gly Tyr Ile Pro Ser Asn Tyr Val Ala Glu Asp Arg Ser Leu
100 105 110

Gln Ala Glu Pro Trp Phe Phe Gly Ala Ile Gly Arg Ser Asp Ala Glu
115 120 125

Lys Gln Leu Leu Tyr Ser Glu Asn Lys Thr Gly Ser Phe Leu Ile Arg
130 135 140

Glu Ser Glu Ser Gln Lys Gly Glu Phe Ser Leu Ser Val Leu Asp Gly
145 150 155 160

Ala Val Val Lys His Tyr Arg Ile Lys Arg Leu Asp Glu Gly Phe
165 170 175

Phe Leu Thr Arg Arg Ile Phe Ser Thr Leu Asn Glu Phe Val Ser
180 185 190

His Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val Lys Leu Gly Lys Pro
195 200 205

Cys Leu Lys Ile Gln Val Pro Ala Pro Phe Asp Leu Ser Tyr Lys Thr
210 215 220

Val Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile Gln Leu Leu Lys Arg
225 230 235 240

Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Glu Gly Leu Trp Asn Asn
245 250 255

Thr Thr Pro Val Ala Val Lys Thr Leu Lys Pro Gly Ser Met Asp Pro
260 265 270

Asn Asp Phe Leu Arg Glu Ala Gln Ile Met Lys Asn Leu Arg His Pro
275 280 285

Lys Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu Glu Asp Pro Ile Tyr
290 295 300

Ile Ile Thr Glu Leu Met Arg His Gly Ser Leu Gln Glu Tyr Leu Gln
305 310 315 320

Asn Asp Thr Gly Ser Lys Ile His Leu Thr Gln Gln Tyr Asp Met Ala
325 330 335

Ala Gln Val Ala Ser Gly Met Ala Tyr Leu Glu Ser Arg Asn Tyr Ile
340 345 350

His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu His Asn Ile
355 360 365

Tyr Lys Val Ala Asp Phe Gly Leu Ala Arg Val Phe Lys Val Asp Asn
370 375 380

Glu Asp Ile Tyr Glu Ser Arg His Glu Ile Lys Leu Pro Val Lys Trp
385 390 395 400

Thr Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe Ser Ile Lys Ser Asp
405 410 415

Val Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile Ile Thr Tyr Gly Lys
420 425 430

Met Pro Tyr Ser Gly Met Thr Gly Ala Gln Val Ile Gln Met Leu Ala
435 440 445

Gln Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys Pro Gln Gln Phe Tyr
450 455 460

Asn Ile Met Leu Glu Cys Trp Asn Ala Glu Pro Lys Glu Arg Pro Thr
465 470 475 480

Phe Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr Phe Glu Thr Asp Ser
485 490 495

Ser Tyr Ser Asp Ala Asn Asn Phe Ile Arg
500 505

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
1 5 10 15
Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
20 25 30
Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
35 40 45
Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
50 55 60
Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
65 70 75 80
Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
85 90 95
Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
100 105 110
Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
115 120 125
Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
130 135 140
Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
145 150 155 160
Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
165 170 175
Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
180 185 190
Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
195 200 205
Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
210 215 220
Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
225 230 235 240
Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
245 250 255
Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
260 265 270
Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
275 280 285
Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
290 295 300
Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
305 310 315 320
Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
325 330 335
Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
340 345 350
Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
355 360 365
Val Trp Ser Phe Gly Ile Leu Trp Glu Ile Tyr Ser Phe Gly Arg
370 375 380
Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
385 390 395 400
Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
405 410 415
Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
420 425 430
Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
435 440 445
His Leu
450

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 659 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
1 5 10 15
Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
20 25 30
Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
35 40 45
Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
50 55 60
Glu Thr Val Val Pro Glu Lys Asn Pro Pro Glu Arg Gln Ile Pro
65 70 75 80
Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
85 90 95
Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
100 105 110
Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
115 120 125
Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
130 135 140
Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
145 150 155 160
Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
165 170 175
Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
180 185 190
Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala
195 200 205
Ala Pro Val Ser Thr Ser Glu Leu Lys Lys Val Val Ala Leu Tyr Asp
210 215 220
Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Asp Glu
225 230 235 240
Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
245 250 255
Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala
260 265 270
Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg
275 280 285
Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
290 295 300
Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
305 310 315 320
Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val
325 330 335
Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
340 345 350
Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
355 360 365
Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
370 375 380
Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
385 390 395 400
Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
405 410 415
Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
420 425 430
Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
435 440 445
Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
450 455 460
Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly

64

465	470	475	480
Cys Leu Leu Asn Tyr	Leu Arg Glu Met	Arg His Arg Phe Gln	Thr Gln
485	490	495	
Gln Leu Leu Glu Met	Cys Lys Asp Val	Cys Glu Ala Met	Glu Tyr Leu
500	505	510	
Glu Ser Lys Gln Phe	Leu His Arg Asp	Leu Ala Ala	Arg Asn Cys Leu
515	520	525	
Val Asn Asp Gln Gly	Val Val Lys Val	Ser Asp Phe Gly	Leu Ser Arg
530	535	540	
Tyr Val Leu Asp Asp	Glu Tyr Thr Ser	Ser Val Gly Ser Lys Phe	Pro
545	550	555	560
Val Arg Trp Ser Pro	Pro Glu Val Leu	Met Tyr Ser Lys Phe	Ser Ser
565	570	575	
Lys Ser Asp Ile Trp Ala	Phe Gly Val	Leu Met Trp Glu	Ile Tyr Ser
580	585	590	
Leu Gly Lys Met Pro	Tyr Glu Arg	Phe Thr Asn Ser	Glu Thr Ala Glu
595	600	605	
His Ile Ala Gln Gly	Leu Arg	Leu Tyr Arg	Pro His Leu Ala Ser Glu
610	615	620	
Lys Val Tyr Thr Ile	Met Tyr Ser	Cys Trp His Glu	Lys Ala Asp Glu
625	630	635	640
Arg Pro Thr Phe Lys	Ile Leu Leu Ser	Asn Ile Leu Asp Val	Met Asp
645	650	655	
Glu Glu Ser			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

*C
cont.*

Met Asn Asn Phe Ile Leu Leu Glu Glu Gln	Leu Ile Lys Lys Ser Gln	
1 5	10 15	
Gln Lys Arg Arg Thr Ser Pro Ser Asn Phe	Lys Val Arg Phe Phe Val	
20	25 30	
Leu Thr Lys Ala Ser Leu Ala Tyr Phe Glu	Asp Arg His Gly Lys Lys	
35	40 45	
Arg Thr Leu Lys Gly Ser Ile Glu Leu Ser	Arg Ile Lys Cys Val Glu	
50	55 60	
Ile Val Lys Ser Asp Ile Ser Ile Pro Cys	His Tyr Lys Tyr Pro Phe	
65	70 75 80	
Gln Val Val His Asp Asn Tyr Leu Leu	Tyr Val Phe Ala Pro Asp Arg	
85	90 95	
Glu Ser Arg Gln Arg Trp Val Leu Ala	Leu Lys Glu Glu Thr Arg Asn	
100	105 110	
Asn Asn Ser Leu Val Pro Lys Tyr His Pro	Asn Phe Trp Met Asp Gly	
115	120 125	
Lys Trp Arg Cys Cys Ser Gln Leu Glu	Lys Leu Ala Thr Gly Cys Ala	
130	135 140	
Gln Tyr Asp Pro Thr Lys Asn Ala Ser	Lys Lys Pro Leu Pro Pro Thr	
145	150 155 160	
Pro Glu Asp Asn Arg Arg Pro Leu Trp	Glu Pro Glu Glu Thr Val Val	
165	170 175	
Ile Ala Leu Tyr Asp Tyr Gln Thr Asn	Asp Pro Gln Glu Leu Ala Leu	
180	185 190	
Arg Arg Asn Glu Glu Tyr Cys Leu	Leu Asp Ser Ser Glu Ile His Trp	
195	200 205	
Trp Arg Val Gln Asp Arg Asn Gly His	Glu Gly Tyr Val Pro Ser Ser	
210	215 220	
Tyr Leu Val Glu Lys Ser Pro Asn Asn	Leu Glu Thr Tyr Glu Trp Tyr	
225	230 235 240	

v6

C

Asn Lys Ser Ile Ser Arg Asp Lys Ala Glu Lys Leu Leu Leu Asp Thr
245 250 255
Gly Lys Glu Gly Ala Phe Met Val Arg Asp Ser Arg Thr Ala Gly Thr
260 265 270
Tyr Thr Val Ser Val Phe Thr Lys Ala Val Val Ser Glu Asn Asn Pro
275 280 285
Cys Ile Lys His Tyr His Ile Lys Glu Thr Asn Asp Asn Pro Lys Arg
290 295 300
Tyr Tyr Val Ala Glu Lys Tyr Val Phe Asp Ser Ile Pro Leu Leu Ile
305 310 315 320
Asn Tyr His Gln His Asn Gly Gly Leu Val Thr Arg Leu Arg Tyr
325 330 335
Pro Val Cys Phe Gly Arg Gln Lys Ala Pro Val Thr Ala Gly Leu Arg
340 345 350
Tyr Gly Lys Trp Val Ile Asp Pro Ser Glu Leu Thr Phe Val Gln Glu
355 360 365
Ile Gly Ser Gly Gln Phe Gly Leu Val His Leu Gly Tyr Trp Leu Asn
370 375 380
Lys Asp Lys Val Ala Ile Lys Thr Ile Arg Glu Gly Ala Met Ser Glu
385 390 395 400
Glu Asp Phe Ile Glu Glu Ala Glu Val Met Met Lys Leu Ser His Pro
405 410 415
Lys Leu Val Gln Leu Tyr Gly Val Cys Leu Glu Gln Ala Pro Ile Cys
420 425 430
Leu Val Phe Glu Phe Met Glu His Gly Cys Leu Ser Asp Tyr Leu Arg
435 440 445
Thr Gln Arg Gly Leu Phe Ala Ala Glu Thr Leu Leu Gly Met Cys Leu
450 455 460
Asp Val Cys Glu Gly Met Ala Tyr Leu Glu Glu Ala Cys Val Ile His
465 470 475 480
Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn Gln Val Ile
485 490 495
Lys Val Ser Asp Phe Gly Met Thr Arg Phe Val Leu Asp Asp Gln Tyr
500 505 510
Thr Ser Ser Thr Gly Thr Lys Phe Pro Val Lys Trp Ala Ser Pro Glu
515 520 525
Val Phe Ser Phe Ser Arg Tyr Ser Ser Lys Ser Asp Val Trp Ser Phe
530 535 540
Gly Val Leu Met Trp Glu Val Phe Ser Glu Gly Lys Ile Pro Tyr Glu
545 550 555 560
Asn Arg Ser Asn Ser Glu Val Val Glu Asp Ile Ser Thr Gly Phe Arg
565 570 575
Leu Tyr Lys Pro Arg Leu Ala Ser Thr His Val Tyr Gln Ile Met Asn
580 585 590
His Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Ala Phe Ser Arg Leu
595 600 605
Leu Arg Gln Leu Ala Glu Ile Ala Glu Ser Gly Leu
610 615 620

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Val Ser Phe Pro Val Lys Ile Asn Phe His Ser Ser Pro Gln
1 5 10 15
Ser Arg Asp Arg Trp Val Lys Lys Leu Lys Glu Glu Ile Lys Asn Asn
20 25 30
Asn Asn Ile Met Ile Lys Tyr His Pro Lys Phe Trp Ala Asp Gly Ser
35 40 45

Wb

Tyr Gln Cys Cys Arg Gln Thr Glu Lys Leu Ala Pro Gly Cys Glu Lys
50 55 60
Tyr Asn Leu Phe Glu Ser Ser Ile Arg Lys Thr Leu Pro Pro Ala Pro
65 70 75 80
Glu Ile Lys Lys Arg Arg Pro Pro Pro Ile Pro Pro Glu Glu Glu
85 90 95
Asn Thr Glu Glu Ile Val Val Ala Met Tyr Asp Phe Gln Ala Thr Glu
100 105 110
Ala His Asp Leu Arg Leu Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu
115 120 125
Lys Asn Asp Leu His Trp Trp Arg Ala Arg Asp Lys Tyr Gly Trp Tyr
130 135 140
Cys Arg Asn Thr Asn Arg Ser Lys Ala Glu Gln Leu Leu Arg Thr Glu
145 150 155 160
Asp Lys Glu Gly Gly Phe Met Val Arg Asp Ser Ser Gln Pro Gly Leu
165 170 175
Tyr Thr Val Ser Leu Tyr Thr Lys Phe Gly Gly Glu Gly Ser Ser Gly
180 185 190
Phe Arg His Tyr His Ile Lys Glu Thr Ala Thr Ser Pro Lys Lys Tyr
195 200 205
Tyr Leu Ala Glu Lys His Ala Phe Gly Ser Ile Pro Glu Ile Ile Glu
210 215 220
Tyr His Lys His Asn Ala Ala Gly Leu Val Thr Arg Leu Arg Tyr Pro
225 230 235 240
Val Ser Thr Lys Gly Lys Asn Ala Pro Thr Thr Ala Gly Phe Ser Tyr
245 250 255
Asp Lys Trp Glu Ile Asn Pro Ser Glu Leu Thr Phe Met Arg Glu Leu
260 265 270
Gly Ser Gly Leu Phe Gly Val Val Arg Leu Gly Lys Trp Arg Ala Gln
275 280 285
Tyr Lys Val Ala Ile Lys Ala Ile Arg Glu Gly Ala Met Cys Glu Glu
290 295 300
Asp Phe Ile Glu Glu Ala Lys Val Met Met Lys Leu Thr His Pro Lys
305 310 315 320
Leu Val Gln Leu Tyr Gly Val Cys Thr Gln Gln Lys Pro Ile Tyr Ile
325 330 335
Val Thr Glu Phe Met Glu Arg Gly Cys Leu Leu Asn Phe Leu Arg Gln
340 345 350
Arg Gln Gly His Phe Ser Arg Asp Met Leu Leu Ser Met Cys Gln Asp
355 360 365
Val Cys Glu Gly Met Glu Tyr Leu Glu Arg Asn Ser Phe Ile His Arg
370 375 380
Asp Leu Ala Ala Arg Asn Cys Leu Val Asn Glu Ala Gly Val Val Lys
385 390 395 400
Val Ser Asp Phe Gly Met Ala Arg Tyr Val Leu Asp Asp Gln Tyr Thr
405 410 415
Ser Ser Ser Gly Ala Lys Phe Pro Val Lys Trp Cys Pro Pro Glu Val
420 425 430
Phe Asn Tyr Ser Arg Phe Ser Ser Lys Ser Asp Val Trp Ser Phe Gly
435 440 445
Val Leu Met Trp Glu Ile Phe Thr Glu Gly Arg Met Pro Phe Glu Lys
450 455 460
Asn Thr Asn Tyr Glu Val Val Thr Met Val Thr Arg Gly His Arg Leu
465 470 475 480
His Arg Pro Lys Leu Ala Thr Lys Tyr Leu Tyr Glu Val Met Leu Arg
485 490 495
Cys Trp Gln Glu Arg Pro Glu Gly Arg Pro Ser Phe Glu Asp Leu Leu
500 505 510
Arg Thr Ile Asp Glu Leu Val Glu Cys Glu Glu Thr Phe Gly Arg
515 520 525

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 537 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
1 5 10 15
Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
20 25 30
Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
35 40 45
Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
50 55 60
Gly Gly Val Asn Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
65 70 75 80
Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
85 90 95
Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
100 105 110
Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
115 120 125
Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
130 135 140
Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
145 150 155 160
Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
165 170 175
Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
180 185 190
Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
195 200 205
Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
210 215 220
Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
225 230 235 240
Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
245 250 255
Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
260 265 270
Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
275 280 285
Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
290 295 300
Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
305 310 315 320
Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
325 330 335
Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
340 345 350
Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
355 360 365
Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
370 375 380
Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
385 390 395 400
Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
405 410 415
Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
420 425 430
Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
435 440 445
Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
450 455 460
Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
465 470 475 480
Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His

	485		490		495										
Glu	Leu	Met	Ile	His	Cys	Trp	Lys	Lys	Asp	Pro	Glu	Glu	Arg	Pro	Thr
	500						505						510		
Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu	Glu	Asp	Tyr	Phe	Thr	Ala	Thr	Glu
	515						520						525		
Pro	Gln	Tyr	Gln	Pro	Gly	Glu	Asn	Leu							
	530					535									

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gln Gly
1 5 10 15
Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
20 25 30
Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn
35 40 45
Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro
50 55 60
Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly
65 70 75 80
Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr
85 90 95
Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn
100 105 110
Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala
115 120 125
Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln
130 135 140
Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg
145 150 155 160
Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu
165 170 175
Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp
180 185 190
Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp
195 200 205
Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln
210 215 220
Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg
225 230 235 240
Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser
245 250 255
Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu
260 265 270
Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr
275 280 285
Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr
290 295 300
Met Ser Pro Glu Ala Phe Leu Glu Ala Gln Ile Met Lys Arg Leu
305 310 315 320
Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
325 330 335
Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
340 345 350
Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
355 360 365
Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn

69

370	375	380
Tyr Ile His Arg Asp Leu Arg Ala Ala Asn	Ile Leu Val Gly Asp Asn	
385 390	395	400
Leu Val Cys Lys Ile Ala Asp Phe Gly	Leu Ala Arg Leu Ile Glu Asp	
405	410	415
Asn Glu Tyr Thr Ala Arg Gln Gly Ala	Lys Phe Pro Ile Lys Trp Thr	
420	425	430
Ala Pro Glu Ala Ala Leu Phe Gly Lys	Phe Thr Ile Lys Ser Asp Val	
435	440	445
Trp Ser Phe Gly Ile Leu Leu Thr	Glu Leu Val Thr Lys Gly Arg Val	
450	455	460
Pro Tyr Pro Gly Met Asn Asn Arg Glu Val	Leu Glu Gln Val Glu Arg	
465 470	475	480
Gly Tyr Arg Met Gln Cys Pro Gly Gly	Cys Pro Pro Ser Leu His Asp	
485	490	495
Val Met Val Gln Cys Trp Lys Arg	Glu Pro Glu Glu Arg Pro Thr Phe	
500	505	510
Glu Tyr Leu Gln Ser Phe Leu Glu Asp	Tyr Phe Thr Ala Thr Glu Pro	
515	520	525
Gln Tyr Gln Pro Gly Asp Asn Gln		
530	535	

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 536 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
1 5 10 15
Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe
20 25 30
Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
35 40 45
Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Glu Pro Lys Leu Phe
50 55 60
Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
65 70 75 80
Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
85 90 95
Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
100 105 110
Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
115 120 125
Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
130 135 140
Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
145 150 155 160
Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
165 170 175
Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
180 185 190
Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
195 200 205
Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
210 215 220
Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
225 230 235 240
Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
245 250 255
Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu

10

260	265	270
Glu Val Lys Leu Gly Gln Gly Cys	Phe Gly Glu Val Trp	Met Gly Thr
275	280	285
Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr		
290	295	300
Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu		
305	310	315
Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro		
325	330	335
Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe		
340	345	350
Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp		
355	360	365
Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn		
370	375	380
Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn		
385	390	395
Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp		
405	410	415
Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr		
420	425	430
Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val		
435	440	445
Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val		
450	455	460
Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg		
465	470	475
Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp		
485	490	495
Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe		
500	505	510
Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro		
515	520	525
Gln Tyr Gln Pro Gly Glu Asn Leu		
530	535	

(2) INFORMATION FOR SEQ ID NO:14:

Cert.
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gly	Cys	Ile	Lys	Ser	Lys	Glu	Asn	Lys	Ser	Pro	Ala	Ile	Lys	Tyr
1				5					10					15	
Arg	Pro	Glu	Asn	Thr	Pro	Glu	Pro	Val	Ser	Thr	Ser	Val	Ser	His	Tyr
				20				25					30		
Gly	Ala	Glu	Pro	Thr	Thr	Val	Ser	Pro	Cys	Pro	Ser	Ser	Ser	Ala	Lys
				35				40				45			
Gly	Thr	Ala	Val	Asn	Phe	Ser	Ser	Leu	Ser	Met	Thr	Pro	Phe	Gly	Gly
				50				55		60					
Ser	Ser	Gly	Val	Thr	Pro	Phe	Gly	Gly	Ala	Ser	Ser	Ser	Phe	Ser	Val
				65				70		75			80		
Val	Pro	Ser	Ser	Tyr	Pro	Ala	Gly	Leu	Thr	Gly	Gly	Val	Thr	Ile	Phe
				85				90				95			
Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	Thr	Glu	Asp	Leu	Ser	Phe
				100				105				110			
Lys	Lys	Gly	Glu	Arg	Phe	Gln	Ile	Ile	Asn	Asn	Thr	Glu	Gly	Asp	Trp
				115				120			125				
Trp	Glu	Ala	Arg	Ser	Ile	Ala	Thr	Gly	Lys	Asn	Gly	Tyr	Ile	Pro	Ser
				130				135			140				
Asn	Tyr	Val	Ala	Pro	Ala	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp	Tyr	Phe

145 150 155 160
Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
165 170 175
Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
180 185 190
Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
195 200 205
Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
210 215 220
Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
225 230 235 240
Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
245 250 255
Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
260 265 270
Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
275 280 285
Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
290 295 300
Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
305 310 315 320
Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
325 330 335
Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
340 345 350
Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
355 360 365
Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
370 375 380
Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
385 390 395 400
Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
405 410 415
Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
420 425 430
Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
435 440 445
Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
450 455 460
Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
465 470 475 480
Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
485 490 495
Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
500 505 510
Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
515 520 525
Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
530 535 540

O
Cmt -

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Cys Val Phe Cys Lys Leu Glu Pro Val Ala Thr Ala Lys
1 5 10 15
Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
20 25 30
His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala

72

C

35 40 45
His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
50 55 60
Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
65 70 75 80
Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
85 90 95
Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
100 105 110
Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile
115 120 125
Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
130 135 140
Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
145 150 155 160
Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
165 170 175
Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
180 185 190
Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr
195 200 205
Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln
210 215 220
His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro
225 230 235 240
Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
245 250 255
Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
260 265 270
Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val
275 280 285
Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu
290 295 300
Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln
305 310 315 320
Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe
325 330 335
Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln
340 345 350
Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu
355 360 365
Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg
370 375 380
Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp
385 390 395 400
Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln
405 410 415
Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe
420 425 430
Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
435 440 445
Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys
450 455 460
Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro
465 470 475 480
Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
485 490 495
Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu
500 505 510
Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln
515 520 525

Thr

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

MB

G

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
1 5 10 15
Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
20 25 30
Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
35 40 45
Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
50 55 60
Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
65 70 75 80
Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
85 90 95
Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
100 105 110
Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
115 120 125
Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
130 135 140
Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
145 150 155 160
Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
165 170 175
Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
180 185 190
Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile
195 200 205
Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys
210 215 220
Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp
225 230 235 240
Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
245 250 255
Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val
260 265 270
Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu
275 280 285
Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg
290 295 300
Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu
305 310 315 320
Tyr Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly
325 330 335
Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala
340 345 350
Glu Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu
355 360 365
Arg Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala
370 375 380
Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg
385 390 395 400
Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn
405 410 415
Phe Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu
420 425 430
Leu Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr
435 440 445
Asn Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg
450 455 460

14

C

435	Asn Ala Asp Val Met Thr Ala	440	Leu Ser Gln Gly Tyr Arg Met Pro Arg	445	
450	455	460			
Val Glu Asn Cys Pro Asp Glu	Leu Tyr Asp Ile Met Lys Met Cys Trp	465	470	475	480
Lys Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val	485	490	495		
Leu Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro	500	505	510		

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Ser Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe
1 5 10 15
Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro
20 25 30
Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn
35 40 45
Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala
50 55 60
Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys
65 70 75 80
Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala
85 90 95
Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val
100 105 110
Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile
115 120 125
Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu
130 135 140
Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser
145 150 155 160
Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His
165 170 175
Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg
180 185 190
Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly
195 200 205
Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys
210 215 220
Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser
225 230 235 240
Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp
245 250 255
Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys
260 265 270
Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met
275 280 285
Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr
290 295 300
Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu
305 310 315 320
Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys
325 330 335
Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu
340 345 350
Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
355 360 365

C
cont.

56

C

385	390	395	400
Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys			
405	410	415	
Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr			
420	425	430	
Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala			
435	440	445	
Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu			
450	455	460	
Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg			
465	470	475	480
Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala			
485	490	495	
Thr Glu Ser Gln Tyr Gln Gln Pro	500	505	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
1 5 10 15
Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
20 25 30
Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
35 40 45
Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
50 55 60
Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
65 70 75 80
Gly Phe Glu Lys Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu
85 90 95
Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
100 105 110
Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
115 120 125
Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
130 135 140
Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
145 150 155 160
Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
165 170 175
Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
180 185 190
Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
195 200 205
Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
210 215 220
Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
225 230 235 240
Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe
245 250 255
Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val
260 265 270
Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu
275 280 285
Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr
290 295 300
Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu
305 310 315 320

290	295	300
Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile	Thr Glu Tyr Met Glu	
305 310	315	320
Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu		
325 330	335	
Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met		
340 345	350	
Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala		
355 360	365	
Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly		
370 375	380	
Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala		
385 390	395	400
Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr		
405 410	415	
Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu		
420 425	430	
Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu		
435 440	445	
Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn		
450 455	460	
Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg		
465 470	475	480
Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp		
485 490	495	
Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro		
500 505		

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly Leu Leu Ser Ser Lys Arg Gln Val Ser Glu Lys Gly Lys Gly
1 5 10 15
Trp Ser Pro Val Lys Ile Arg Thr Gln Asp Lys Ala Pro Pro Pro Leu
20 25 30
Pro Pro Leu Val Val Phe Asn His Leu Ala Pro Pro Ser Pro Asn Gln
35 40 45
Asp Pro Asp Glu Glu Arg Phe Val Val Ala Leu Phe Asp Tyr Ala
50 55 60
Ala Val Asn Asp Arg Asp Leu Gln Val Leu Lys Gly Glu Lys Leu Gln
65 70 75 80
Val Leu Arg Ser Thr Gly Asp Trp Trp Leu Ala Arg Ser Leu Val Thr
85 90 95
Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe Val Ala Pro Val Glu Thr
100 105 110
Leu Glu Val Glu Lys Trp Phe Phe Arg Thr Ile Ser Arg Lys Asp Ala
115 120 125
Glu Arg Gln Leu Leu Ala Pro Met Asn Lys Ala Gly Ser Phe Leu Ile
130 135 140
Arg Glu Ser Glu Ser Asn Lys Gly Ala Phe Ser Leu Ser Val Lys Asp
145 150 155 160
Ile Thr Thr Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Ser Leu
165 170 175
Asp Asn Gly Gly Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Thr Leu
180 185 190
Gln Ala Leu Val Gln His Tyr Ser Lys Lys Gly Asp Gly Leu Cys Gln
195 200 205
Lys Leu Thr Leu Pro Cys Val Asn Leu Ala Pro Lys Asn Leu Trp Ala

Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Lys Asn
245 250 255
Asn Met Lys Val Ala Ile Lys Thr Leu Lys Glu Gly Thr Met Ser Pro
260 265 270
Glu Ala Phe Leu Gly Glu Ala Asn Val Met Lys Thr Leu Gln His Glu
275 280 285
Arg Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Pro Ile Tyr Ile
290 295 300
Val Thr Glu Tyr Met Ala Arg Gly Cys Leu Leu Asp Phe Leu Lys Thr
305 310 315 320
Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg Leu Ile Asp Met Ser Ala
325 330 335
Gln Val Ala Glu Gly Met Ala Tyr Ile Glu Arg Met Asn Ser Ile His
340 345 350
Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Glu Thr Leu Cys Cys
355 360 365
Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Asp Ser Glu Tyr Thr
370 375 380
Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala
385 390 395 400
Ile His Phe Gly Val Phe Thr Ile Lys Ala Asp Val Trp Ser Phe Gly
405 410 415
Val Leu Leu Met Val Ile Val Thr Tyr Gly Arg Val Pro Tyr Pro Gly
420 425 430
Met Ser Asn Pro Glu Val Ile Arg Ser Leu Glu His Gly Tyr Arg Met
435 440 445
Pro Cys Pro Glu Thr Cys Pro Pro Glu Leu Tyr Asn Asp Ile Ile Thr
450 455 460
Glu Cys Trp Arg Gly Arg Pro Glu Glu Arg Pro Thr Phe Glu Phe Leu
465 470 475 480
Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Glu
485 490 495
Leu Gln Pro

*C
cont.*
(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAATTCCCA CAGNGACTTN GCNGCNAG

28

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCGA ANGTCCANAC GTCNGA

26